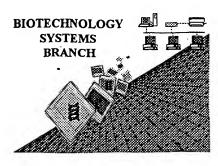# RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/006,972_

Source: _CIPE_

Date Processed by STIC: _12/20/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: **patin21help@uspto.gov** or phone **703-306-4119 (R. Wax)**
PATENTIN 3.0 e-mail help: **patin3help@uspto.gov** or phone **703-306-4119 (R. Wax)**

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
   http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by the treatment given to all mail coming via the Brentwood Mail Facility.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom, including:
1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , **EFS Submission User Manual** - ePAVE)
2. U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
    U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, 1911 South Clark Street, Crystal Mall One, Sequence Information, Arlington, VA 22202
              Or
    U.S. Patent and Trademark Office, 2011 South Clark Place, Customer Window, Box Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, Virginia 22202
4. Federal Express Delivery, 2011 South Clark Street, Crystal Plaza 2, Room 1B03-Mailroom, Box Sequence, Arlington, VA 22202

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _10/006,972_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWAR

1_____Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2_____Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3_____Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4_____Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5_____Variable Length

Sequence(s)_____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6_____PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)_____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7_____Skipped Sequences
(OLD RULES)

Sequence(s)_____missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8_____Skipped Sequences
(NEW RULES)

Sequence(s)_____missing. If Intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number   _follow this format_
000

9_____Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.

10_____Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11_____Use of <220>

Sequence(s)_____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12_____PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13_____Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

OIPE

```
            RAW SEQUENCE LISTING              DATE: 12/20/2001
            PATENT APPLICATION:  US/10/006,972   TIME: 13:02:41

            Input Set : A:\RTS-0335 Sequence Listing.txt
            Output Set: N:\CRF3\12202001\J006972.raw

     3 <110> APPLICANT: Kenneth W. Dobie
     5 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPID SCRAMBLASE 3 EXPRESSION
     7 <130> FILE REFERENCE: RTS-0335
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/006,972
C--> 9 <141> CURRENT FILING DATE: 2001-12-04
     9 <160> NUMBER OF SEQ ID NOS: 94
    12 <210> SEQ ID NO: 1
    13 <211> LENGTH: 20
    14 <212> TYPE: DNA
    15 <213> ORGANISM: Artificial Sequence
    17 <220> FEATURE:
    19 <223> OTHER INFORMATION: Antisense Oligonucleotide
    21 <400> SEQUENCE: 1
    22 tccgtcatcg ctcctcaggg                                       20
    25 <210> SEQ ID NO: 2
    26 <211> LENGTH: 20
    27 <212> TYPE: DNA
    28 <213> ORGANISM: Artificial Sequence
    30 <220> FEATURE:
    32 <223> OTHER INFORMATION: Antisense Oligonucleotide
    34 <400> SEQUENCE: 2
    35 atgcattctg cccccaagga                                       20
    38 <210> SEQ ID NO: 3
    39 <211> LENGTH: 1680
    40 <212> TYPE: DNA
    41 <213> ORGANISM: Homo sapiens
    43 <220> FEATURE:   ← delete - duplicated below
    45 <220> FEATURE:
    46 <221> NAME/KEY: CDS
    47 <222> LOCATION: (144)...(1031)
    49 <400> SEQUENCE: 3
    50 cggggccggg gtccgagctc gggcccgcct ccgcctccgc cagctcctgt gagctgccga   60
    52 gtgctaggca cccgggctct tctggggggct ccagaactaa gccacccaga caccatcatc  120
    54 tcgaaaaccc cagcccttct ccc atg gca ggc tac ttg ccc ccc aaa ggc tac  173
    55                         Met Ala Gly Tyr Leu Pro Pro Lys Gly Tyr
    56                          1               5                  10
    58 gcc cct tcg ccc cca cct ccc tac cct gtc acc cct ggg tac ccg gag    221
    59 Ala Pro Ser Pro Pro Pro Pro Tyr Pro Val Thr Pro Gly Tyr Pro Glu
    60               15                  20                  25
    62 ccg gcg cta cat cct ggg ccc ggg cag gcg cca gtg ccc gcc cag gta    269
    63 Pro Ala Leu His Pro Gly Pro Gly Gln Ala Pro Val Pro Ala Gln Val
    64               30                  35                  40
    66 cct gcc cca gct ccc ggc ttc gcc ctc ttc ccc tcg cct ggc ccc gtg    317
    67 Pro Ala Pro Ala Pro Gly Phe Ala Leu Phe Pro Ser Pro Gly Pro Val
    68               45                  50                  55
    70 gcc ttg ggg tct gct gcc ccc ttc ttg cca ctg cca ggg gtg cct tct    365
    71 Ala Leu Gly Ser Ala Ala Pro Phe Leu Pro Leu Pro Gly Val Pro Ser
```

```
72      60                      65           .          70
74 ggc ctc gaa ttc ctg gtg cag att gat cag att ttg att cac cag aag      413
75 Gly Leu Glu Phe Leu Val Gln Ile Asp Gln Ile Leu Ile His Gln Lys
76  75                      80                   85                   90
78 gct gag cga gtg gaa acg ttc cta ggc tgg gag acc tgt aat cgg tat      461
79 Ala Glu Arg Val Glu Thr Phe Leu Gly Trp Glu Thr Cys Asn Arg Tyr
80                      95                   100                   105
82 gaa ctg cgc tct ggg gcc ggg cag ccc ctg ggt cag gcg gcc gag gag      509
83 Glu Leu Arg Ser Gly Ala Gly Gln Pro Leu Gly Gln Ala Ala Glu Glu
84                      110                  115                  120
86 agc aac tgc tgc gcc cgt ctg tgc tgt ggc gcc cgc cgg ccg ctg cgt      557
87 Ser Asn Cys Cys Ala Arg Leu Cys Cys Gly Ala Arg Arg Pro Leu Arg
88              125                  130                  135
90 gtc cgc ctg gcc gac ccc ggg gac cgt gag gtg ctg cgt ttg ctc cgc      605
91 Val Arg Leu Ala Asp Pro Gly Asp Arg Glu Val Leu Arg Leu Leu Arg
92      140                  145                  150
94 ccg ctg cac tgt ggc tgc agc tgc tgc ccc tgt ggc ctc cag gag atg      653
95 Pro Leu His Cys Gly Cys Ser Cys Cys Pro Cys Gly Leu Gln Glu Met
96 155                     160                  165                  170
98 gaa gta cag gct cca cca ggc acc acc att ggc cac gtg cta cag acc      701
99 Glu Val Gln Ala Pro Pro Gly Thr Thr Ile Gly His Val Leu Gln Thr
100                     175                  180                  185
102 tgg cat ccc ttc ctc ccc aag ttc tcc atc cag gat gcc gat cgc cag     749
103 Trp His Pro Phe Leu Pro Lys Phe Ser Ile Gln Asp Ala Asp Arg Gln
104                     190                  195                  200
106 aca gtc ttg cga gtg gtg ggg ccc tgc tgg acc tgt ggc tgt ggc aca     797
107 Thr Val Leu Arg Val Val Gly Pro Cys Trp Thr Cys Gly Cys Gly Thr
108              205                  210                  215
110 gac acc aac ttt gag gtg aag act cgg gat gaa tcc cgc agt gtg ggc     845
111 Asp Thr Asn Phe Glu Val Lys Thr Arg Asp Glu Ser Arg Ser Val Gly
112      220                  225                  230
114 cgc atc agc aag cag tgg ggg ggc ctg gtc cga gaa gcc ctc aca gat     893
115 Arg Ile Ser Lys Gln Trp Gly Gly Leu Val Arg Glu Ala Leu Thr Asp
116 235                     240                  245                  250
118 gca gat gac ttt ggc cta cag ttc ccg ctg gac ctg gat gtg agg gtg     941
119 Ala Asp Asp Phe Gly Leu Gln Phe Pro Leu Asp Leu Asp Val Arg Val
120                     255                  260                  265
122 aag gct gtg ctg ctg gga gcc aca ttc ctc att gac tac atg ttc ttt     989
123 Lys Ala Val Leu Leu Gly Ala Thr Phe Leu Ile Asp Tyr Met Phe Phe
124              270                  275                  280
126 gag aag cga gga ggc gct ggg ccc tct gcc atc acc agt tag aggccaccat 1041
127 Glu Lys Arg Gly Gly Ala Gly Pro Ser Ala Ile Thr Ser
128              285                  290                  295
130 ggtgtgagga gaccatcacc tcgaccagaa ctccagatgg tcacctgccc tggcccctcc 1101
132 tctgggcagc ccctttcctc catgtacact gcaggggaca gaaggggggc cccatcccta 1161
134 ccctactccc tggccgcctg cccctgtggt tcccaaggag gggtatgtat gagagccgct 1221
136 ctcctgctac ctcccaccac tgtcccagca gtccctcggc acacaggcat atcagctttc 1281
138 acactttccc catgcactct ctcccacccc cttccagggc ctctgctcca aggaggcct 1341
140 ctggaaccca ggactctggg gttttacaag agggctgggg tgtggaaggg caagctgcac 1401
```

```
                 RAW SEQUENCE LISTING              DATE: 12/20/2001
                 PATENT APPLICATION:  US/10/006,972    TIME: 13:02:41

                 Input Set : A:\RTS-0335 Sequence Listing.txt
                 Output Set: N:\CRF3\12202001\J006972.raw

142  caaagacggt ggatatagcc accgccccc cgccgctgcc tagcatctgc ttggccaatt  1461
144  agttcagcct cagaccatgg cactttgagg gggtctctac ctccccatca acagctgcag  1521
146  ggggacccca gtgccaactt cctctcccac tagggccctg ccttcagctg gtgcttgctg  1581
148  cgattcctgt gccttatgta actgcccttc cttcccttgc cctaggaaaa aggctgcatc  1641
150  tttatatgtt acattcatat aaactttgta actttttgg                         1680
153  <210> SEQ ID NO: 4
154  <211> LENGTH: 20
155  <212> TYPE: DNA
156  <213> ORGANISM: Artificial Sequence
158  <220> FEATURE:
160  <223> OTHER INFORMATION: PCR Primer
162  <400> SEQUENCE: 4
163  gtccgagaag ccctcacaga                                               20
166  <210> SEQ ID NO: 5
167  <211> LENGTH: 19
168  <212> TYPE: DNA
169  <213> ORGANISM: Artificial Sequence
171  <220> FEATURE:
173  <223> OTHER INFORMATION: PCR Primer
175  <400> SEQUENCE: 5
176  gccttcaccc tcacatcca                                                19
179  <210> SEQ ID NO: 6
180  <211> LENGTH: 27
181  <212> TYPE: DNA
182  <213> ORGANISM: Artificial Sequence
184  <220> FEATURE:
186  <223> OTHER INFORMATION: PCR Probe
188  <400> SEQUENCE: 6
189  cagatgactt tggcctacag ttcccgc                                       27
192  <210> SEQ ID NO: 7
193  <211> LENGTH: 19
194  <212> TYPE: DNA
195  <213> ORGANISM: Artificial Sequence
197  <220> FEATURE:
199  <223> OTHER INFORMATION: PCR Primer
201  <400> SEQUENCE: 7
202  gaaggtgaag gtcggagtc                                                19
205  <210> SEQ ID NO: 8
206  <211> LENGTH: 20
207  <212> TYPE: DNA
208  <213> ORGANISM: Artificial Sequence
210  <220> FEATURE:
212  <223> OTHER INFORMATION: PCR Primer
214  <400> SEQUENCE: 8
215  gaagatggtg atgggatttc                                               20
218  <210> SEQ ID NO: 9
219  <211> LENGTH: 20
220  <212> TYPE: DNA
221  <213> ORGANISM: Artificial Sequence
```

RAW SEQUENCE LISTING   DATE: 12/20/2001
PATENT APPLICATION: US/10/006,972   TIME: 13:02:41

Input Set : A:\RTS-0335 Sequence Listing.txt
Output Set: N:\CRF3\12202001\J006972.raw

```
223 <220> FEATURE:
225 <223> OTHER INFORMATION: PCR Probe
227 <400> SEQUENCE: 9
228 caagcttccc gttctcagcc                                        20
231 <210> SEQ ID NO: 10
232 <211> LENGTH: 596
233 <212> TYPE: DNA
234 <213> ORGANISM: Homo sapiens
236 <220> FEATURE:
238 <221> NAME/KEY: exon:exon junction
239 <222> LOCATION: (333)...(334)
240 <223> OTHER INFORMATION: exon 5:exon 6b
242 <221> NAME/KEY: exon:exon junction
243 <222> LOCATION: (423)...(424)
244 <223> OTHER INFORMATION: exon 6b:exon 7
247 <400> SEQUENCE: 10
248 ttggggtctg ctgcccctt cttgccactg ccagggtgcc ttctggcctc gaattcctgg    60
250 tgcagattga tcagattttg attcaccaga aggctgagcg agtggaaacg ttcctagtgc   120
252 tgggagacct gtaatcggta tgaactgcgc tctggggcct gggcagcccc tgggtcaggc   180
254 ggccgaggag agcaactgct gcgcccgtct gtgctgtggc tgcccgccgg cctgctgcgt   240
256 gtccgcctgg ccgaccccgg ggaccgtgag gtgctgcgtt tgctccgccc gctgcactgt   300
258 ggctgcagct gctgcccctg tggcctccag gagttctcca tccaggatgc cgatcgccag   360
260 acagtcttgc gagtggtggg gccctgctgg acctgtggct gtggcacaga caccaacttt   420
262 gaggtgaaga ctcgggatga atcccgcagt gtgggccgca tcagcaagca gtgtgggggg   480
264 cctggtccga gaagccctca cagatgcaga tgactttggc ctacagttcc cgctggacct   540
266 ggatgtgagg gtgaaggctg tgctgctggg agccacattc ctcatttgac tactgt        596
269 <210> SEQ ID NO: 11
270 <211> LENGTH: 000
271 <212> TYPE: DNA
272 <213> ORGANISM: Homo sapiens
274 <220> FEATURE:
276 <400> SEQUENCE: 11
277 000
279 <210> SEQ ID NO: 12
280 <211> LENGTH: 000
281 <212> TYPE: DNA
282 <213> ORGANISM: Homo sapiens
284 <220> FEATURE:
286 <400> SEQUENCE: 12
287 000
289 <210> SEQ ID NO: 13
290 <211> LENGTH: 000
291 <212> TYPE: DNA
292 <213> ORGANISM: Homo sapiens
294 <220> FEATURE:
296 <400> SEQUENCE: 13
297 000
299 <210> SEQ ID NO: 14
300 <211> LENGTH: 20
```

[handwritten annotations: "W", "OK", "do not show these in an intentionally skipped sequence (see item 8 on Error Summary Sheet for valid format)", "OK"]

The types of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

```
301 <212> TYPE: DNA
302 <213> ORGANISM: Artificial Sequence
304 <220> FEATURE:
306 <223> OTHER INFORMATION: Antisense Oligonucleotide
308 <400> SEQUENCE: 14
309 cggcagctca caggagctgg                                      20
312 <210> SEQ ID NO: 15
313 <211> LENGTH: 20
314 <212> TYPE: DNA
315 <213> ORGANISM: Artificial Sequence
317 <220> FEATURE:
319 <223> OTHER INFORMATION: Antisense Oligonucleotide
321 <400> SEQUENCE: 15
322 gcactcggca gctcacagga                                      20
325 <210> SEQ ID NO: 16
326 <211> LENGTH: 20
327 <212> TYPE: DNA
328 <213> ORGANISM: Artificial Sequence
330 <220> FEATURE:
332 <223> OTHER INFORMATION: Antisense Oligonucleotide
334 <400> SEQUENCE: 16
335 tgcctagcac tcggcagctc                                      20
338 <210> SEQ ID NO: 17
339 <211> LENGTH: 20
340 <212> TYPE: DNA
341 <213> ORGANISM: Artificial Sequence
343 <220> FEATURE:
345 <223> OTHER INFORMATION: Antisense Oligonucleotide
347 <400> SEQUENCE: 17
348 tggcttagtt ctggagcccc                                      20
351 <210> SEQ ID NO: 18
352 <211> LENGTH: 20
353 <212> TYPE: DNA
354 <213> ORGANISM: Artificial Sequence
356 <220> FEATURE:
358 <223> OTHER INFORMATION: Antisense Oligonucleotide
360 <400> SEQUENCE: 18
361 tggtgtctgg gtggcttagt                                      20
364 <210> SEQ ID NO: 19
365 <211> LENGTH: 20
366 <212> TYPE: DNA
367 <213> ORGANISM: Artificial Sequence
369 <220> FEATURE:
371 <223> OTHER INFORMATION: Antisense Oligonucleotide
373 <400> SEQUENCE: 19
374 tcgagatgat ggtgtctggg                                      20
377 <210> SEQ ID NO: 20
378 <211> LENGTH: 20
379 <212> TYPE: DNA
```

VERIFICATION SUMMARY   DATE: 12/20/2001
PATENT APPLICATION: US/10/006,972   TIME: 13:02:42

      Input Set : A:\RTS-0335 Sequence Listing.txt
      Output Set: N:\CRF3\12202001\J006972.raw

```
L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:238 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
L:242 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
L:277 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (11) SEQUENCE:
L:287 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (12) SEQUENCE:
L:297 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (13) SEQUENCE:
L:1193 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (82) SEQUENCE:
L:1206 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (83) SEQUENCE:
L:1219 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (84) SEQUENCE:
L:1232 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (85) SEQUENCE:
L:1245 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (86) SEQUENCE:
L:1284 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (89) SEQUENCE:
L:1297 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (90) SEQUENCE:
L:1310 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (91) SEQUENCE:
```